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EXAMINER	
WESSENDORF, TERESA D	

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1639	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/582,050	LU ET AL.	
	Examiner	Art Unit	
	TERESA WESSENDORF	1639	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *24 March 2010*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-4,27-36 and 45-74* is/are pending in the application.

4a) Of the above claim(s) *1-4,35,36 and 45-74* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *27-34* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

Newly submitted claims 45-74 directed to an invention that is independent or distinct from the invention originally claimed for the following reasons: these claims e.g., claim 48 are drawn to methods of transfecting a population of cells i.e., cellular library to determine its effect on the phenotype of the cell. These methods are distinct from the originally presented and prosecuted method claims of making **non-cellular** nucleic acid.

Since applicant has received an action on the merits for the originally presented invention, this invention has been constructively elected by original presentation for prosecution on the merits. Accordingly, claims 45-74 are withdrawn from consideration as being directed to a non-elected invention. See 37 CFR 1.142(b) and MPEP § 821.03.

Status of Claims

Claims 1-4, 27-36 and 45-74 are pending in the application.

Claims 1-4, 35-36 and 45-74 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention.

Claims 5-26 and 37-44 have been cancelled.

Claims 27-34 are under examination.

Withdrawn Objection/Rejection

In view of the newly submitted abstract of the disclosure, the objection to the specification is withdrawn.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Claim Rejections - 35 USC § 101

Claims 27-34, as amended, are rejected under 35 U.S.C. 101 because the claimed invention lacks patentable utility for reasons of record as reiterated below.

The claim method of producing a non-cellular nucleic acid library, said method comprising: (a) dividing an initial set of a plurality of separate nucleic acids into two or more pooled collections of nucleic acids having an initial sequence representation profile, wherein each pooled collection includes not more than about 100 distinct nucleic acids; (b) amplifying each of said pooled collections to produce two or more amplified pooled collections; and (c) combining said two or more amplified

pooled collections to produce said non-cellular nucleic acid library, wherein said non-cellular nucleic acid library has a sequence representation profile that is substantially the same as said initial sequence representation profile lacks have a patentable utility.

The claim method of making a non-cellular library from a set of known collections of nucleic acids e.g., EST (expressed sequence tags) produces an intermediate product (library), which do not have a specific, disclosed utility. The court in *Brenner v. Manson*, 148 U.S.P.Q. 689 (1966), expressed the opinion that all chemical compounds/methods are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S.C. §101, which requires that an invention must have either an immediately apparent or fully disclosed "real world" utility. The court held that:

> The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility. . . . [u]nless and until a process is refined and developed to this point-where specific benefit exists in currently available form-there is insufficient justification for permitting an applicant to engross what may prove to be a broad field. . . . a patent is not a hunting license. . . .[i]t is not a reward for the search, but compensation for its successful conclusion.

> Congress intended that no patent be granted on a chemical compound whose sole 'utility' consists of its potential role as an object of use-testing." *Brenner*, 148 USPQ at 696.

The method has no patentable utility since it simply collects data from a known collection of data and dividing it into smaller portions to obtain the initial compound from which the (fragment) sets are derived/obtained. It is not apparent from the specification' Examples any specific utility for the claim method. Even assuming that a library is obtained still the library, an intermediate product, has to undergo screening in the hope that the obtained product has a patentable utility. The claim process of collecting/compiling products produced from the method has not been refined and developed to the point-where specific benefit exists in currently available form. There is insufficient justification for permitting an applicant to engross what may prove to be a broad field.

The disclosure at e.g., page 40, lines 17-20 states the utility of the EST-based approach of the subject invention for **global** inactivation of host genes, where the subject methodology is useful as a general loss-of-function genetic screen. The above utility is not a specific utility. Thus applicants have only conclude

the disclosed general use for its claimed DNA library of plasmids but not specific ones that satisfy § 101. The claimed DNA library of plasmids can be used only to gain further information about the underlying genes. The claimed DNA library themselves are not an end of [applicant's] research effort, but only tools to be used along the way in the search for a practical utility. Applicants do not identify the function for the underlying DNA library of non-cellular nucleic acids. Absent such identification, the claimed library has not been researched and understood to the point of providing an immediate, well- defined, real world benefit to the public meriting the grant of a patent. The claim is to an intermediate product for use in making a final product that has no specific, substantial and credible utility. See MPEP 2107.01.

A patent is not a hunting license. . . .[i]t is not a reward for the search, but compensation for its successful conclusion. Further, the Court approved a rejection for failure to disclose any utility for a compound where the compound was undergoing screening for possible compounds the utility of which has also not been identified. Brenner, 148 USPQ at 690.

Thus, it is not readily apparent from the disclosure as to the specific utility of the library produced by the method.

Response to Arguments

Applicant's arguments filed 3/24/10 have been fully considered but they are not persuasive.

Applicants note that the specification teaches that a nucleic acid library is "a collection of nucleic acids, where each constituent nucleic acid member of the library is of known sequence and corresponds to a known chromosomal transcript" (p. 6, I. 30-32) Hence, and contrary to the Examiner's assertions, the pending claimed methods are not for "simply collect[ing] data from a known collection of data and dividing it into smaller portions."

In reply, the fact still remains that the method produces a library (i.e., collection of nucleic acids, as asserted) which does not have a specific or substantial utility.

Applicants argue that nucleic acid libraries have a patentable utility in and of themselves, namely as tools that

enable researchers to analyze the roles of nucleic acids represented therein in modulating various biological processes, e.g., cellular growth, sensitivity to infectious agents or chemical substances, the ability of a cell to differentiate, cell morphology, cellular response to changes in the environment, etc. This utility is asserted in the subject patent specification, page 20, line 30 - page 22, I. 32.

In reply, none of the aforementioned utility e.g., cellular growth would be considered a specific or substantial as required under the 35 USC 101 statue.

Applicants assert that an exemplary use for one such nucleic acid library produced by the pending claimed method is set forth in great detail on page 32, line 24 - page 41, line 27. In this working example, Applicants identified a problem to be solved, namely identifying the mechanistic basis of cellular sensitivity to anthrax, and then uses a nucleic acid library produced by the claimed method for its investigation. Accordingly, the product of the claimed method is a research tool which finds use in, for example, screening assays to analyze nucleic acids for their roles as candidate agents in modulating biological processes. With regard to research tools,

in particular research tools in the context of screening assays, applicants rely on the MPEP 2107.01, Part I. Applicants state that the MPEP dictates that "screening assays and nucleotide sequence techniques have a clear, specific and unquestionable utility". Applicants respectfully submit that if screening assays themselves have utility, so, too must libraries used in those screening assays and methods for making such libraries. Furthermore, since the instant claims are directed to methods of making tools useful in screening assays, the subject matter of the instant claims, i.e. methods of making the libraries used in these assays, must, too, have a clear, specific and unquestionable utility.

In reply, as acknowledged by applicants above the nucleic acid library is used to **investigate** the mechanistic(?) bases of cellular sensitivity to anthrax.

Furthermore, the instant claim is not to a method of screening rather to a method of making an intermediate compound i.e., a nucleic acid collection or library. The research tools cited by applicants such as screening assays have a clear, specific and unquestionable utility. Inventions that have a specifically identified utility must be distinguished from those whose utility which requires further research to identify or

reasonably confirm. Research tools (such as screening assays and etc.) are useful in the sense that they can be used in conjunction with other method steps to evaluate materials other than themselves or to arrive at some result. The claimed combinatorial libraries are not research tools in this sense. Rather, they are themselves the subject of basic research, whose usefulness or lack thereof has yet to be established. Merely labeling the instant libraries as "research tools" does not impart the specific utility required by this statute.

MPEP 2106[R6] A states:

> The purpose of this [utility] requirement is to limit patent protection to inventions that possess a certain level of "real world" value, as opposed to subject matter that represents nothing more than an idea or concept, or is simply a starting point for **future investigation** or research (Brenner v. Manson, 383 U.S. 519,528-36, 148 USPQ 689, 693-96 (1966); In re Fisher, 421 F.3d 1365, 76 USPQ2d1225 (Fed. Cir. 2005); In re Ziegler, 992 F.2d 1197, 1200-03, 26 USPQ2d 1600, 1603-06 (Fed. Cir. 1993)). (Emphasis added.)

See applicants' statement as to the used of the nucleic acid library for investigative purposes. As stated above, a patent is not a hunting license [i]t is **not a reward** for the search, but compensation for its successful conclusion. Further, the Court approved a rejection for failure to

disclose any utility for a compound (herein, nucleic acid library) where the compound was undergoing screening for possible compounds the utility of which has also not been identified. Brenner, 148 USPQ at 690.

Applicants state that the USPTO has issued a number of patents in the last year alone for methods of making and/or using nucleic acid libraries including patents issued by the present Examiner. Applicants state that it would not be inconsistent with current USPTO practice to find that the products of the claimed methods, namely, nucleic acid libraries, do in fact have a specific, substantial and credible utility and that, as such, the methods of the pending claims for preparing this products meet the criteria for utility under 35 U.S.C. §101.

In reply, each case is treated on its own merits. Notably, the patents issued by the present examiner are mostly drawn to screening specific library. The claims of the issued patent are unlike the instant method of making EST library. The instant EST sequence forms only a part of a whole nucleic acid sequence. It is not apparent whether applicants are claiming the whole sequence of the EST or EST gene as part of a nucleic acid

sequence. The single species obtained from a consortium does not disclose whether EST as a gene of a nucleic acid or the whole nucleic acid sequence itself. Hence, it is not apparent from the instant EST library whether in fact this is where the utility of the whole (unsequenced or sequenced) nucleic acid resides. It is clear that further research is required before the claimed nucleic library produced by the method would be of any benefit to the public. The courts have decided that a utility which requires or constitutes carrying out further research to identify or reasonably confirm a "real world" context of use lacks substantial utility.

> 'The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility. . . . [u]nless and until a process is refined and developed to this point-where specific benefit exists in currently available form-there is insufficient justification for permitting an applicant to engross what may prove to be a broad field." Brenner v. Manson, 383 US 519 (1966).

Claim Rejections - 35 USC § 112

Claims 27-34, as amended, are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to

reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention for reasons of record as repeated below.

Written Descritpion

Claim 27, for example, is drawn to a method of producing a non-cellular nucleic acid library, said method comprising: (a) dividing an initial set of a plurality of separate nucleic acids into two or more pooled collections of nucleic acids having an initial sequence representation profile, wherein each pooled collection includes not more than about 100 distinct nucleic acids; (b) amplifying each of said pooled collections to produce two or more amplified pooled collections; and (c) combining said two or more amplified pooled collections to produce said non\-cellular nucleic acid library, wherein said non-cellular nucleic acid library has a sequence representation profile that is substantially the same as said initial sequence representation profile..

The specification fails to describe the genus claim method of producing any kind or type of generic non-cellular nucleic acid library of such enormous scope. A claim to such enormous scope should have a corresponding written description that would

lead one skilled to the said enormous genus claim. However, the specification at e.g.., page 11, lines 10-13 merely provides definitions for each of the claim term. The detail description at e.g., page 33 is drawn to an EST library obtained from human genes from IMAGE consortium. The specification also does not describe this consortium from which the EST human genes are obtained. Li et al (US 2002/0168640) at page 8, [0107] states that "... it is important to understand that in any library system encoded by oligonucleotide synthesis one cannot have complete control over the codons that will eventually be incorporated into the peptide structure. This is especially true in the case of codons encoding stop signs…" Due to the high level of DNA binding specificity of transcription factors, each transcription factor will typically bind to a different DNA sequence. In some instances, a related family of transcription factors may bind to the same DNA sequence. Selection of the sequences used in the hybridization probes may be based on the different tfs that one wishes to detect in a sample. This in turn may depend on the type of organism, cell, or disease state one wished to identify and/or monitor the gene expression of. ***It is noted that different organisms will also express different activated transcription factors and the expression level could be biased.*** Thus, the general statements in the specification are

not an adequate written description of the invention. A written description should be specific, not generic since a genus is highly variant, that would lead a skilled artisan to the invention.

Response to Arguments

Applicants submit that although the specification only provides a working example using a human EST collection, there is no reason to believe that other sets of separate nucleic acids could not similarly be divided into at least two pooled collections of nucleic acids having an initial sequence representation profile, wherein each pooled collection includes not more than about 100 distinct nucleic acids; (b) amplified as pooled collections to produce two or more amplified pooled collections; and (c) combined to produce said non-cellular nucleic acid library, wherein the non-cellular nucleic acid library has a sequence representation profile that is substantially the same as said initial sequence representation profile, as recited by the pending claims. The Examiner has provided no evidence to suggest that nucleic acids other than the ESTs described in the working examples would not be amenable

to such manipulation, e.g. pipetting, or amplification, or pipetting again. Absent such evidence, one of ordinary skill in the art would fully expect that sets of other separate nucleic acids could also be used in the pending claimed method, and thus, that non-cellular nucleic acid libraries representative of other sets of separate nucleic acids could, in fact, be generated from any initial set of separate nucleic acids. Furthermore, it was well within the skill of the ordinarily skilled artisan to acquire such sets of nucleic acids, for example by performing RT-PCR on cells of interest to them and preparing a bacterial library of the cDNAs; or by preparing select nucleic acids individually, e.g. to form a collection of nucleic acids representative of a gene family; or by purchasing one of many commercially available nucleic acid collections, e.g. ESTs from IMAGE or Riken.

In reply, the specification and applicants' arguments are no more than general statements or steps for any type of EST. The applicability of which has been exemplified for a single EST obtained from a consortium. It cannot be ascertained from applicants' statements or specification whether any other species can be used to represent the enormous scope of the genus claim. The specification does not describe in detail how one can

obtain EST besides the disclosed (not described) consortorium. Importantly, whether the product(s) of the subsets of library would be functional. (Please see the 101 rejection above). Absent any showing to the contrary and indication that the single species would be representative for the huge scope of any EST using the broad process steps, the genus claim is not adequately described. The law clearly indicates that a patent specification must describe the claimed invention in sufficient detail (not in general terms). An applicant shows possession of the claimed invention by describing the claimed invention with all of its limitations using such descriptive means as words, structures and formulas to show that the invention is complete. Lockwood v. American Airlines, Inc., 107 F.3d 1565, 1572, 41 USPQM 1961, 1966 (Fed. Cir. 1997); MPEP 2163. The general statements in the specification are therefore not a detail description of the invention. A "written description of an invention involving a chemical genus, like a description of a chemical species, requires a precise definition, such as by structure, formula [or] chemical name of the claimed subject matter sufficient to distinguish it from other materials". University of California v. Eli Lilly and Col, 43 USPQ 2d 1398, 1405(1997), quoting Fiers V. Revel, 25 USPQ 2d 1601-1616 (Fed. Cir. 1993.

Applicant, at the time of filing, is deemed to have not invented species sufficient to constitute the genus by virtue of having disclosed a single species when … the evidence indicates ordinary artisans could not predict the operability in the invention of any species other than the one disclosed. In re Curtis, 354 F.3d 1347, 1358, 69 USPQ2d 1274, 1282 (Fed. Cir. 2004).

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 27-34 rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention for reasons of record as reiterated below only for the **MAINTAINED REJECTIONS.**

1. Claim 27 is indefinite as to the metes and bound of the claim "more'. It is suggested to change "more" to -at least-.

Response to Arguments

Applicants state that claim 27 has been amended to recite "at least."

In reply this phrase still appears in claim 27, steps b) and c), "two or more" amplified products.

Claim Rejections - 35 USC § 102

I. Claims 27-34, as amended, are rejected under 35 U.S.C. 102(e) as being anticipated by Edwards et al (7235381) for reasons of record as repeated below.

Edwards discloses at e.g., EXAMPLE 1 a method comprising preparing mRNA derived from different tissues. In Example 3 Edwards discloses that from mRNA template (initial set as claimed) two strands of cDNA are obtained a first and a second strand of the cDNA. In Example 4, Edwards teaches that the cDNA undergoes size fractionation and fractions corresponding to cDNAs of more than 150 bp were pooled. The cDNA was directionally cloned into the vector. The ligation mixture was

electroporated into bacteria and propagated under appropriate antibiotic selection.

Edwards discloses at e.g., Example 7 a method by which 5'ESTs are isolated from other cDNA or genomic DNA libraries. The full-length cDNAs are then separated into several fractions according to their sizes using techniques familiar to those skilled in the art. For example, electrophoretic separation may be applied in order to yield 3 or 6 different fractions. Following gel extraction and purification, the cDNA fractions are subcloned into appropriate vectors transformed into competent bacteria and propagated under appropriate antibiotic conditions. Subsequently, plasmids containing tagged full-length cDNAs are positively selected.

Claim 31 is disclosed by Edwards at e.g., col. 5, lines 15-25, backbone molecules nucleic acids such as integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched 5' ESTs represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

Claim 29 is disclosed by Edwards at e.g., col. 59, the multiple copies result from amplification of a chromosomal sequence.

Claims 33 and 34 are disclosed by Edwards at e.g., col.8, lines 15-25, the term "fragments of EST-related nucleic acids" means fragments comprising at least 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive nucleotides of the EST-related nucleic acids to the extent that fragments of these lengths are consistent with the lengths of the particular EST-related nucleic acids being referenced. In particular, fragments of EST-related nucleic acids refer to "polynucleotides described in Table II," "polynucleotides described in Table III," and "polynucleotides described in Table IV." The present invention also includes the sequences complementary to the fragments of the EST-related nucleic acids.

Response to Arguments

Applicants submit that Edwards et al. does not anticipate the pending claims because Edwards et al. does not disclose amplifying pooled collections of nucleic acids to produce two or more pooled collections, or pooling these pools. Edwards et al. teaches making RNA from various tissues (Example 1) or from 5' ESTs from cDNA or genomic libraries (Example 7), synthesizing

cDNA from that RNA (Example 2) and cloning that cDNA (Example 3). Edwards teaches fractionating that cDNA by size and pooling the cDNAs greater than 150bp (Example 4); selecting those cDNAs with a 5' oligo tag (Example 5) and transforming them into bacteria. However, nowhere in Edwards et al's procedure does Edwards et al. disclose amplifying pooled collections of initial sets of nucleic acids, or pooling amplified products; for example, Edwards et al. does not amplify the pools of cDNAs greater than 150bp. Edwards et al. is silent on amplification.

In reply, attention is drawn to Edwards' reference at e.g., col. 59, which recites that the multiple copies result from amplification of a chromosomal sequence.

II. Claims 27, 30, 32, 33 and 34 are rejected under 35 U.S.C. 102(b) as anticipated by Chengtao et al (Chinese Journal of Biochemistry, 1999.) for reasons of record as repeated below.

Chengtao discloses a method of obtaining from an initial set of malaria epitopes sets of two or more fragments, amplifying said sets of two or more nucleic acid and combining the two to produce the original nucleic acid. See paragraph

2.1.1, Results section, which describes two synthetic chains of fragment I were inserted between *Bcl* I and *Bam*H I of the carrier VR1012 immediately after annealing, resulting in a clone that included the start codon. Using the T4 DNA polymerase or PCR method, fragments 2, 6, 8 underwent extension and filling in after each corresponding fragment was annealed, and were inserted into the carrier VR1012 after double enzyme digestion by *Bcl* I and *Bam*H or *Bgl* II, resulting in clones that contained fragments 2, 6, and 8. At paragraph 2.1.2 Chengtao discloses the combination of the individual cloned fragments tandemized and further sequencing results proved that the sequence of the constructed polyvalent recombinant DNA is entirely correct by matching with the original set.

Response to Arguments

Applicants state that Chengtao et al. teaches annealing synthetic single strand DNA to make double strand fragments 2, 6, or 8, filling in the ends and cutting with enzymes, and ligating into vector VR1012 to form monoclones of 2, 6, or 8 (2.1.1). Chengtao et al. teaches cutting out these DNA fragments from the monoclones with enzymes, and recloning the three different fragments into 1 vector (2.1.2). However, nowhere in Chengtao et al's procedure does Chengtao et al. disclose pooling initial sets of distinct nucleic acids, amplifying the pooled

collections, and pooling amplified products; for example, Chengtao et al does not pool the DNA fragments cut from the monoclones, or amplify those fragments, or pool those amplified products. Chengtao et al. is silent on pooling and amplification. Because Chengtao et al. does not disclose every step of the pending claimed method,

In reply, attention is drawn again to the Chengtao's teachings above which discloses a method of obtaining from an initial set of malaria epitopes sets of two or more fragments, amplifying said sets of two or more nucleic acid and combining the two to produce the original nucleic acid. See paragraph 2.1.1, Results section.

Accordingly, the specific process steps of Chengtao employing the specific nucleic acid from an initial set of Malaria epitopes anticipates the broad claimed method with no defined sequence but broadly any kind of EST sequence.

III. Claims 27-28, 30 and 32 are rejected under 35 U.S.C. 102(b) as anticipated by Okazaki et al (Nature, 2002) for reasons as stated in the previous office action and reiterated below.

Okasaki at e.g., page 568 col. 1, a method useful to detect and classify evolutionarily related groups of domains for which there is a known structural representative. The ancestral domain from each superfamfly represents a genetic building block. These building blocks have been duplicated, recombined to create the proteins that are currently observed in the genome. At col. 2, Okazaki discloses functional proteins less than 100 amino acids in length were annotated only if they showed significant homology to known proteins from other species or members of gene families. On the basis of these stringent criteria, only 376 proteins of less than 100 amino acids were annotated.

Okazaki at e.g., page 571 under the Methods section discloses a method comprising constructing an initial set of library and extracting a genomic region of >100 bases. The sets were paired and amplified. See further page 565, col. 2, wherein Okazaki refers to reference 21 for the pattern of expression.

Response to Arguments

Applicants submit that Okazaki et al. does not disclose amplifying pools of nucleic acids or pooling amplified pooled collections. Okazaki et al. teaches dividing an initial set of

cDNAs into 171,144 clusters based on sequence similarity (paragraph bridging p. 563 and 564), and sequencing cDNAs representative of those clusters. However, nowhere in Okazaki et al's procedure does Okazaki et al. disclose amplifying the pooled collections of initial sets of nucleic acids, or pooling those amplified products. Okazaki et al. is silent on amplification.

In reply, attention is drawn to the disclosure of Okazaki et al which teaches that set were paired and amplified. Furthermore, it is unclear as to how Okazaki could produce the genomic region if it is not amplified. Thus, the express teachings of Okazaki using specific cDNA populations fully meet the broad claimed process steps of making broad ESTs.

No claim is allowed.

Conclusion

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL.** See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened

statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

This application contains claims 1-4, 35-36 and 45-74 drawn to non-elected inventions. A complete reply to the final rejection must include cancellation of nonelected claims or other appropriate action (37 CFR 1.144) See MPEP § 821.01.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to TERESA WESSENDORF whose telephone number is (571)272-0812. The examiner can normally be reached on flexitime.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low can be reached on 571-272-0951. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/TERESA WESSENDORF/
Primary Examiner, Art Unit 1639